



In the Specification

Please amend the title as follows:

Novel methods ~~of~~ for detection and diagnosing of breast cancer ~~, compositions,~~
~~and methods of screening for breast cancer modulators.~~

Please insert the following new paragraph on page 1, after line 8 and before the heading of "BACKGROUND OF THE INVENTION":

RELATED APPLICATIONS

This application is a continuation-in-part of U.S. Patent Application Ser No. 09/525,361 filed March 15, 2000, which is a continuation-in-part of U.S. Patent Application Ser No. 09/453,137 filed December 2, 1999, and this application is a continuation-in-part of international application PCT/US00/06952, filed March 15, 2000; each of which is incorporated herein by reference in its entirety.

Please amend the paragraph starting on page 9, line 9 as follows:

In a preferred embodiment, breast cancer sequence are those that are up-regulated in breast cancer; that is, the expression of these genes is higher in breast carcinoma as compared to normal breast tissue. "Up-regulation" as used herein means at least about a 50% increase, preferably a two-fold change, more preferably at least about a three fold change, with at least about five-fold or higher being preferred. All accession numbers herein are for the GenBank sequence datanase and the sequences of the accession numbers are hereby expressly incorporated by rerference. GenBank is known in the art, see, e.g., Benson, DA, et al., Nucleic Acids Research 26:1-7 (1998) ~~and~~ <http://www.ncbi.nlm.nih.gov/>. In addition, these genes are found to be expressed in a limited amount or not at all in bladder, bone marrow, brain, colon, fibroblasts, heart, kidney, liver, lung, muscle, pancreas, prostate, skin, small intestine, spleen, stomach and testes.

Please amend the paragraph starting on page 13, line 4 as follows:

Another example of a useful algorithm is the BLAST algorithm, described in Altschul et al., J. Mol. Biol. 215, 403-410, (1990) and Karlin et al., PNAS USA 90:5873-5787 5877 (1993). A particular useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul et al., Methods in Enzymology, 266: 460-480 (1996) [~~http://blast.wustl.edu/blast/READ.html~~]. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span =1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the “longer” sequence in the aligned region. The “longer” sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-Blast-2 to maximize the alignment score are ignored).